

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/589,594
Source: IFWP
Date Processed by STIC: 8/28/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

DATE: 08/28/2006

PATENT APPLICATION: US/10/589,594

TIME: 10:43:27

Input Set : A:\082368-008900US.txt

Output Set: N:\CRF4\08282006\J589594.raw

4 <110> APPLICANT: Nakamura, Yusuke
 5 Furukawa, Yoichi
 7 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING COLORECTAL CANCERS
 10 <130> FILE REFERENCE: 082368-008900US
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/589,594
 C--> 12 <141> CURRENT FILING DATE: 2006-08-15
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002145
 13 <151> PRIOR FILING DATE: 2004-02-24
 15 <160> NUMBER OF SEQ ID NOS: 23
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2624
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (294)...(1688)
 28 <400> SEQUENCE: 1

29 ggcacgaggg gccgacgca gcgcgcgcgt tcgcttcagc tgctagctgg cccaagggag 60
 30 gcgaccgcgg aggggtggcga ggggcggcca ggaccgcag ccccggggcc gggccggtcc 120
 31 ggaccgccag ggagggcagg tcagtgggca gatcgcgctc gcgggattca atctctgccc 180
 32 gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcaccgc gctgggcgcc 240
 33 tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg 296
 34 Met
 35 1

37 tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag 344
 38 Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
 39 5 10 15

41 cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
 42 Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
 43 20 25 30

45 att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
 46 Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
 47 35 40 45

49 aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc 488
 50 Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
 51 50 55 60 65

53 ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac 536
 54 Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
 55 70 75 80

57 aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act 584
 58 Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
 59 85 90 95

see p. 8

**Does Not Comply
Corrected Diskette Needed**

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Input Set : A:\082368-008900US.txt

Output Set: N:\CRF4\08282006\J589594.raw

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61 acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg 632
62 Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg
63          100          105          110
65 agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa 680
66 Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys
67      115          120          125
69 caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa 728
70 Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys
71 130          135          140          145
73 acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac 776
74 Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn
75          150          155          160
77 tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct 824
78 Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala
79          165          170          175
81 ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc 872
82 Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val
83          180          185          190
85 tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg 920
86 Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr
87      195          200          205
89 gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca 968
90 Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser
91 210          215          220          225
93 gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg 1016
94 Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu
95          230          235          240
97 gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag 1064
98 Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln
99          245          250          255
101 ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa 1112
102 Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln
103          260          265          270
105 aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca 1160
106 Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala
107      275          280          285
109 gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa 1208
110 Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln
111 290          295          300          305
113 aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag 1256
114 Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu
115          310          315          320
117 aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca 1304
118 Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr
119          325          330          335
121 tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa 1352
122 Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu
123          340          345          350
125 caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac 1400

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126 Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp
127      355                      360                      365
129 cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga 1448
130 Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
131 370                      375                      380                      385
133 aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat 1496
134 Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
135                      390                      395                      400
137 gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa 1544
138 Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
139                      405                      410                      415
141 aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc 1592
142 Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
143                      420                      425                      430
145 aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc 1640
146 Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
147                      435                      440                      445
149 act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag 1688
150 Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys *
151 450                      455                      460
153 caaaataagt atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg 1748
154 ggcattttga attatatatt tcacattttg cataaaactg cctatctacc ttgacactc 1808
155 cagcatgcta gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac 1868
156 ctccctgaca tgggttcac tcaaggctgca atgacagaat gtggtgagca gcgtctactg 1928
157 agactactaa cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcagggttatt 1988
158 gctaattgggt taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca 2048
159 aagataatta accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac 2108
160 ctacaatcct aattttgatg tccattgtta agagggtggtg atagatacta tttttttttt 2168
161 catattgtat agcgggttatt agaaaagttg gggattttct tgatctttat tgctgcttac 2228
162 cattgaaact taaccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt 2288
163 ttgaggcata atcttaagtg gccacacaca atgttttctc ttatgtttatc tggcagtaac 2348
164 tgtaacttga attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat 2408
165 aaacccatgt agccctctca tttgattgac agtatttttag ttatttttgg cattcttaaa 2468
166 gctgggcaat gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt 2528
167 ttgtaaacca aaaactttta aattttcttca ggttttctaa catgcttacc actgggctac 2588
168 tgtaaataag aaaagaataa aattatttaa tgtttt 2624
170 <210> SEQ ID NO: 2
171 <211> LENGTH: 464
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 2
176 Met Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser
177 1 5 10 15
178 Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
179 20 25 30
180 Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
181 35 40 45
182 Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
183 50 55 60

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RAW SEQUENCE LISTING

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184 Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
185 65                               70                               75                               80
186 Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
187                               85                               90                               95
188 Thr Thr Ala Leu Leu Glu Gln Leu Glu Thr Thr Arg Glu Gly Glu
189                               100                              105                              110
190 Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
191                               115                              120                              125
192 Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
193                               130                              135                              140
194 Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
195 145                               150                               155                               160
196 Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
197                               165                               170                               175
198 Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
199                               180                              185                              190
200 Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
201                               195                              200                              205
202 Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
203                               210                              215                              220
204 Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
205 225                               230                               235                               240
206 Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
207                               245                              250                              255
208 Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
209                               260                              265                              270
210 Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
211                               275                              280                              285
212 Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
213                               290                              295                              300
214 Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
215 305                               310                               315                               320
216 Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
217                               325                              330                              335
218 Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
219                               340                              345                              350
220 Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
221                               355                              360                              365
222 Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
223                               370                              375                              380
224 Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
225 385                               390                               395                               400
226 His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
227                               405                              410                              415
228 Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
229                               420                              425                              430
230 Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
231                               435                              440                              445
232 Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys

```

RAW SEQUENCE LISTING

DATE: 08/28/2006

PATENT APPLICATION: US/10/589,594 .

TIME: 10:43:27

Input Set : A:\082368-008900US.txt

Output Set: N:\CRF4\08282006\J589594.raw

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233      450      455      460
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 22
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
243      RT-PCR
245 <400> SEQUENCE: 3
246 acaacagcct caagatcatc ag                      22
248 <210> SEQ ID NO: 4
249 <211> LENGTH: 20
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
255      RT-PCR
257 <400> SEQUENCE: 4
258 ggtccaccac tgacacgttg                      20
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 23
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
267      RT-PCR
269 <400> SEQUENCE: 5
270 agagatccga agagctctta tct                      23
272 <210> SEQ ID NO: 6
273 <211> LENGTH: 21
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
279      RT-PCR
281 <400> SEQUENCE: 6
282 gatgctcagt ggctggatac t                      21
284 <210> SEQ ID NO: 7
285 <211> LENGTH: 24
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
291      RT-PCR
293 <400> SEQUENCE: 7
294 cgaaagcttc agagatgtct tcca                      24
296 <210> SEQ ID NO: 8
297 <211> LENGTH: 27
298 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
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DATE: 08/28/2006
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Input Set : A:\082368-008900US.txt
Output Set: N:\CRF4\08282006\J589594.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 489,490,491,492

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/589,594

DATE: 08/28/2006

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Input Set : A:\082368-008900US.txt

Output Set: N:\CRF4\08282006\J589594.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:485 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:489 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:480

<210> 23
<211> 5089
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized vector sequence

<221> misc_feature

<222> (489)...(492)

<223> n = GAP

<400> 23

"n" can only represent a single nucleotide, nothing else